

SEQUENCE LISTING

<110> DAVIS, SIMON

<120> RECEPTOR MODULATORS

<130> ISI.103

<140> US 10/585,491

<141> 2006-07-07

<150> PCT/GB05/000099

<151> 2005-01-10

<150> GB 0400440.4

<151> 2004-01-09

<150> US 60/536,354

<151> 2004-01-14

<160> 61

<170> PatentIn version 3.2

<210> 1

<211> 220

<212> PRT

<213> Homo sapiens

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<222> (1)..(220)

<223> HUMAN CD28

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
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Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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<223> CD28/Fc fusion protein

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Ile Asn Ala Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala
 20 25 30

Tyr Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe
 35 40 45

Ser Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val
 50 55 60

Glu Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr
 65 70 75 80

Ser Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val
 85 90 95

Thr Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe
 100 105 110

Cys Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys

115					120					125						
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130					135					140						
Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro	Leu	Val	Pro	Arg	Gly	Ser	Gly	
145					150					155					160	
Ser	Lys	Pro	Ser	Ile	Ser	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	Phe	Ile	
165					170					175						
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	
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Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	
195					200					205						
Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	
210					215					220						
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	
225					230					235					240	
Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	
245					250					255						
Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	
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Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	
275					280					285						
Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	
290					295					300						
Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	
305					310					315					320	
Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp	Gly	
325					330					335						
Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	
340					345					350						
Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His	Asn	
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Xaa
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 <211> 31
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<210> 14
 <211> 34
 <212> DNA
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ctactatcta gattatttac caggagagtg ggag

34

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<211> 1514

<212> DNA

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ctcaacttat tcccttcaat tcaagtaaca ggaaacaaga ttttggtgaa gcagtcgccc	180
atgctttagt cgtacgacaa tgcggtcaac cttagctgca agtattccta caatctcttc	240
tcaagggagt tccgggcata ctttcacaaa ggactggata gtgctgtgga agtctgtgtt	300
gtatatggga attactccca gcagcttcag gtttactcaa aaacgggggt caactgtgat	360
gggaaattgg gcaatgaatc agtgacattc tacctccaga atttgtatgt taaccaaaca	420
gatatttact tctgcaaaat tgaagttatg tatectcttc cttacctaga caatgagaag	480
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc	540
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ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctctctg	660
cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag	720
ccctatgccc caccacgaga cttcgcagcc tategctcct gacacggacg cctatccaga	780
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ccatctccag ccggccacct cagccccctgt tgggccacca atgccaatTT ttctcgagtg	900
actagaccaa atatcaagat cattttgaga ctctgaaatg aagtaaaaga gatttcctgt	960
gacaggccaa gtcttacagt gccatggccc acattccaac ttaccatgta cttagtgact	1020
tgaactgaaa gttagggtag aaaacaaaaa gggagtggat tctgggagcc tcttcccttt	1080
ctcaactcacc tgcacatctc agtcaagcaa agtgtggtat ccacagacat tttagttgca	1140

gaagaaaggc taggaaatca ttcccttttgg ttaaatgggt gtttaatctt ttggtttagtg 1200
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 aaacactgtc tcccactcat gaaatgagcc acgtagtcc tatttaaatgc tgttttccctt 1320
 tagtttagaa atacatagac attgtctttt atgaattctg atcatattta gtcattttga 1380
 ccaaattgagg gatttgggtca aatgagggat tccctcaaag caatatcagg taaaccaagt 1440
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 gaataaaaata gttc 1514

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 cgggcatccc ttcacaaagg actggatagt gctgtggaag tctgtgttgt atatgggaat 240
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 aatgaatcag tgacattcta cctccagaat ttgtatgtta accaaacaga tatttaactc 360
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 ttcaaattgca ggggtcaacag tgcagcttcc cctgcoccca tcgagaaaac catctccaaa 840
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 gccaaaggata aagtcagttc gacctgcagc ataacagact tcttccctga agacattact 960

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gtggagtggc agtggaatgg gcagccagcg gagaactaca agaactca gccatcatg 1020
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<210> 17
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          20          25          30

Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
          35          40          45

Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
          50          55          60

Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65          70          75          80

Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
          85          90          95

Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
          100          105          110

Ile Tyr Val
          115

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<223> HUMAN ICOS

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Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
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Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
20 25 30

Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
35 40 45

Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
50 55 60

Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65 70 75 80

His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
85 90 95

Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile
100 105 110

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Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu
20 25 30

Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala
35 40 45

Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg Val
50 55 60

Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg Ala
65 70 75 80

Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu Ala
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Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg

100

105

110

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 Val Thr Phe Thr Cys Arg Ser Ser Gln Thr Ile Gly Thr Tyr Leu Asn
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Phe Ala
 35 40 45
 Ala Ser Ser Leu Leu Asn Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Pro Tyr Thr
 85 90 95
 Phe Gly Gln Gly Thr Arg Leu Glu Met Lys
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 Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser Val Asn Asn Leu Gln Trp
 20 25 30
 Phe His Gln Asn Pro Trp Gly Gln Leu Ile Asn Leu Phe Tyr Ile Pro
 35 40 45

Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser Ala Thr Thr Val Ala Thr
50 55 60

Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser Ser Gln Thr Thr Asp Ser
65 70 75 80

Gly Val Tyr Phe Cys Ala Ala Leu Asp Leu Trp Gly Gly Ala Asp Gly
85 90 95

Leu Thr Phe Gly Lys Gly Thr His Leu Ile Ile Gln
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<223> HUMAN BTLA

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Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala Asn Arg Pro His
20 25 30

Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val Lys Leu Glu Asp
35 40 45

Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn Ile Ser Phe Phe Ile Leu
50 55 60

His Phe Glu Pro Met Leu Pro Asn Asp Asn Gly Ser Tyr Arg Cys Ser
65 70 75 80

Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser Thr Thr Leu Tyr
85 90 95

Val Thr

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Ser Pro Met Leu Val
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Pro Ala Val Val Leu
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Tyr Glu Met Phe Ile
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Ala Val Asn Leu Ser
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Gly Ile Ala Ser Phe Val
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Gly Val Gln Ile Leu
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<210> 31

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<212> PRT

<213> Artificial sequence

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Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
1 5 10

<210> 32

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Phe Phe Leu Tyr Asn
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Pro Ala Leu Leu Val Val
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Gln Ser Glu His Ser Ile
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Asp Asn Ala Thr Phe
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Asp Pro Phe Glu Leu
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Arg Met Ser Pro Ser Asn Gln Thr Asp Lys
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Lys Leu Asn Gly
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Asn Asp Ser Gly Thr Tyr
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Asn Asp Asn Gly Ser Tyr
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Leu Arg Ala Glu Leu Arg
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Thr Thr Leu Tyr Val Thr
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Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe
 1 5 10 15

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Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
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Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys
 1 5 10 15

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Leu Ala Ala Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg
 1 5 10 15